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Fig. 1

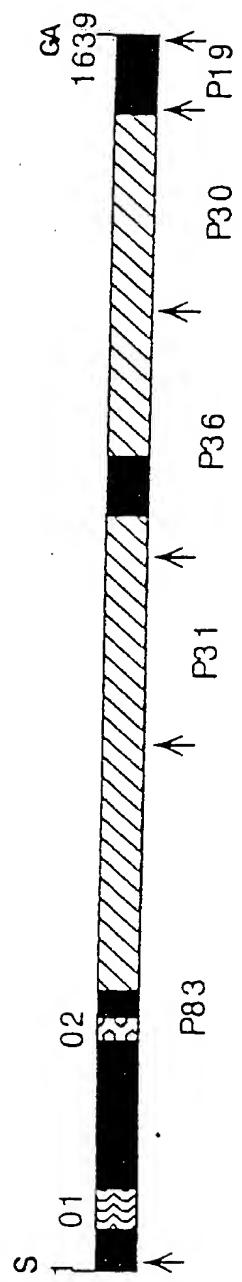
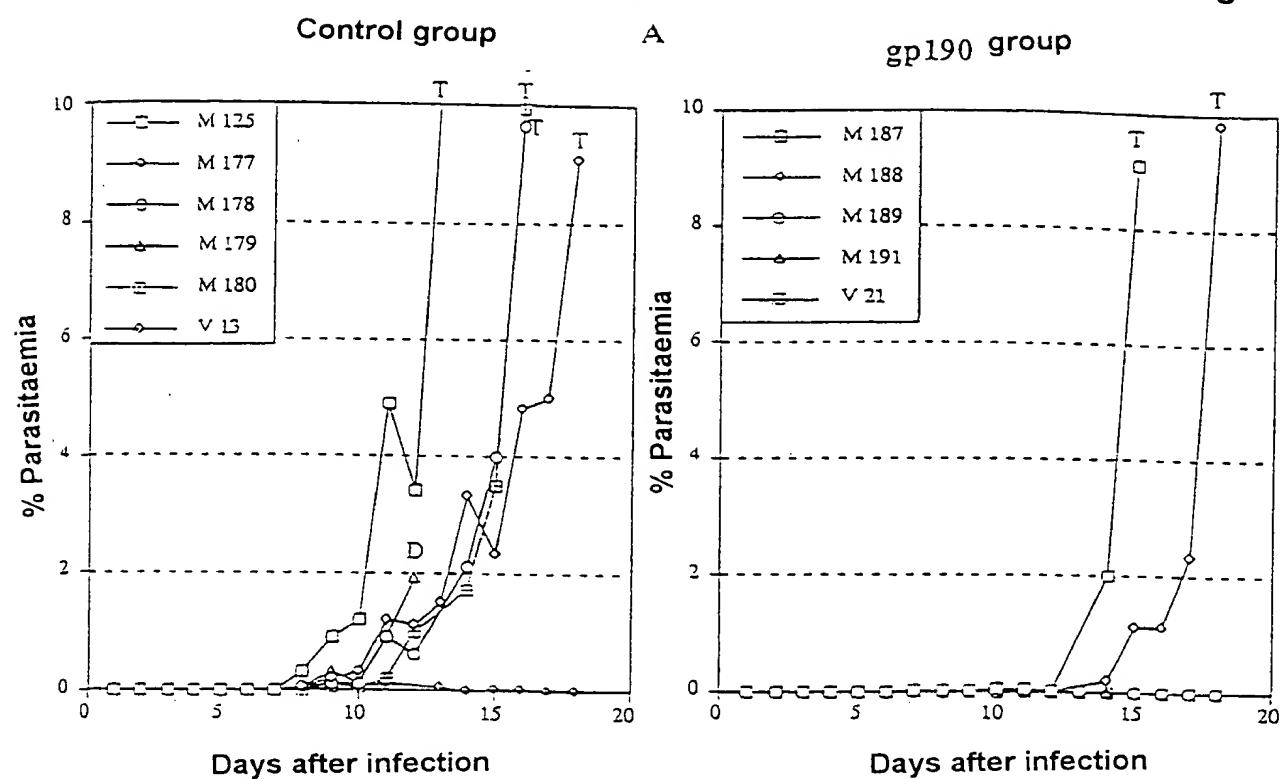
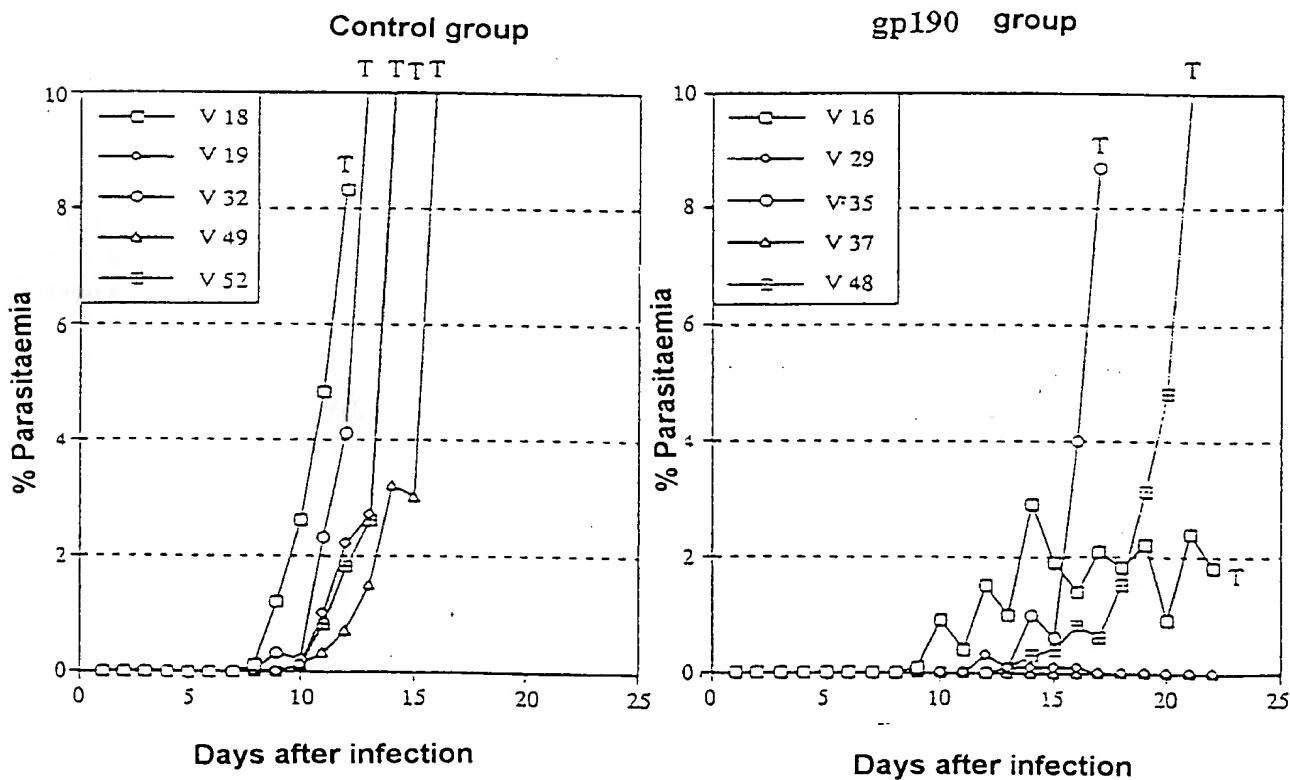


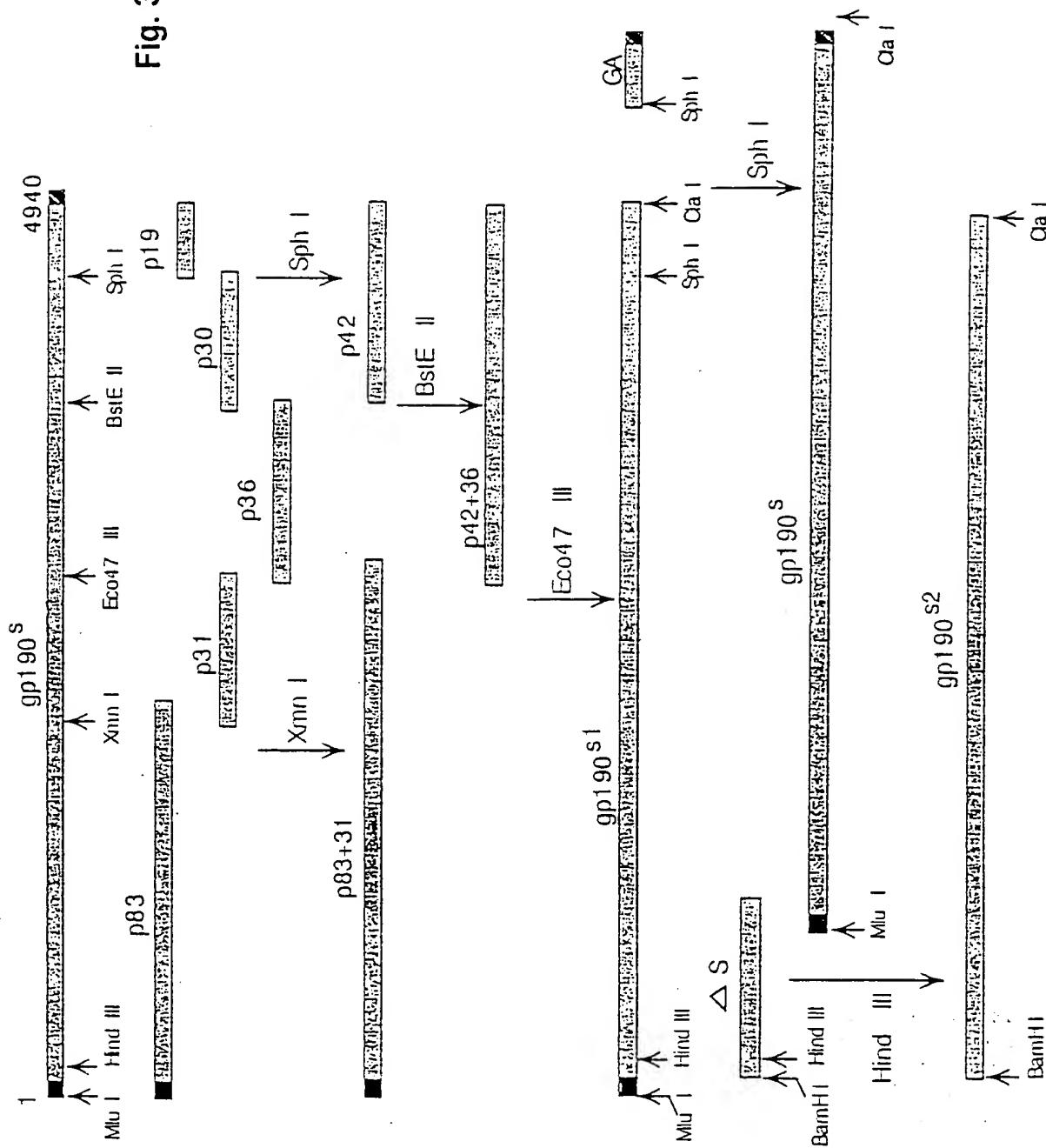
Fig. 2

**B**

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Fig. 3A



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Fig. 3B

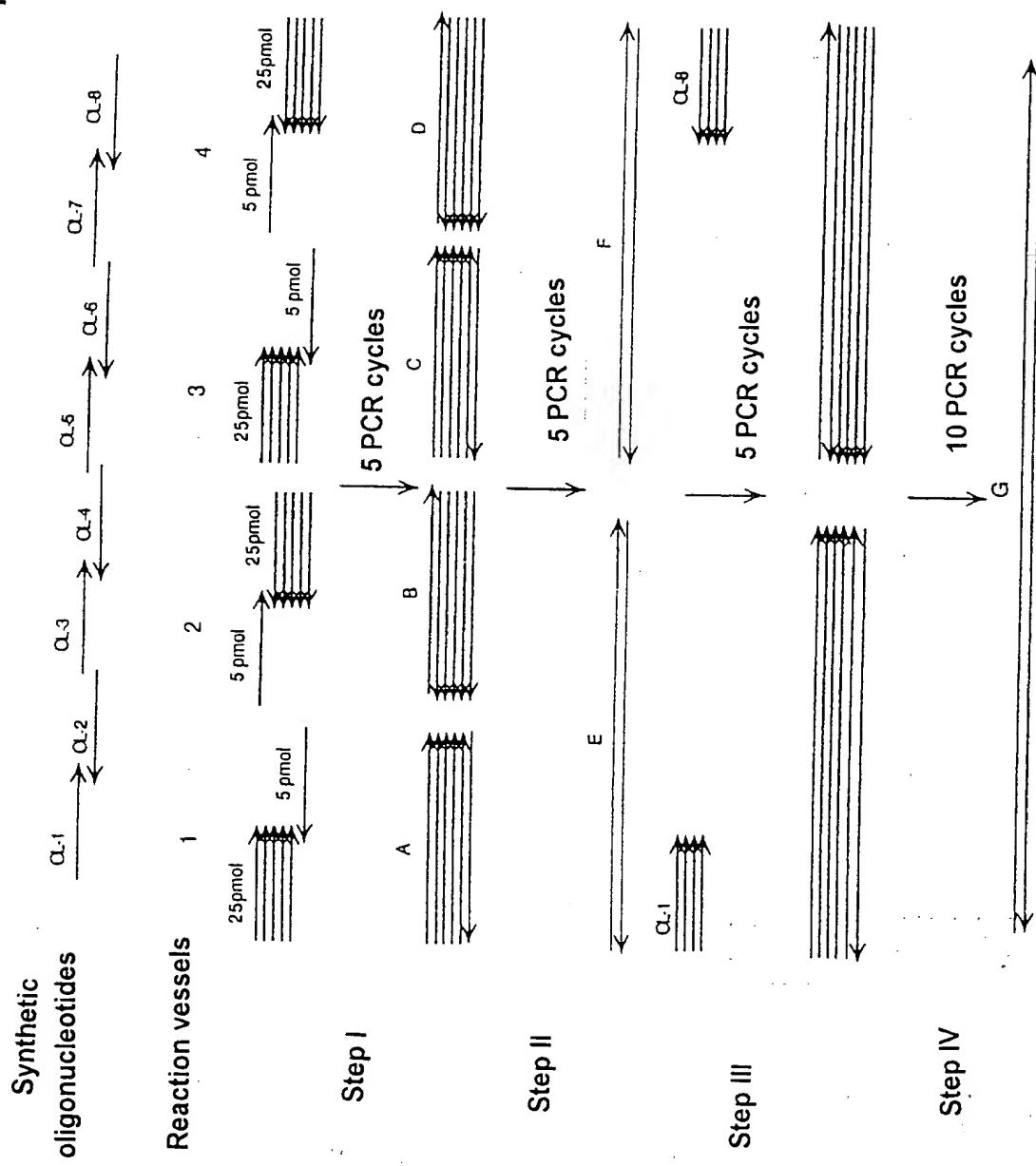


Fig. 3C

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DNA sequence of the native (gp190n) and of the synthetic gene (gp190s) for gp190 from ECG-1

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AS	H N L E K L T K A L K Y M E D Y S L R N I V V E K E L K Y Y	567
gp190 ⁿ	A T A A A A A T T A A T A A T A T A	
gp190 ^s	CATAATCTTGAGAAGCTCACCAAAAGCTCTTAAGTATATGGAGGACTATTCTCTCGGAAACATTGTGAGAAGAAACTAAAGTATTAC	1710
AS	K N L I S K I E N E I E T I V E N I K K D E E Q L F E K K I	597
gp190 ⁿ	A T A C A A T T A A T A A T A A A C T A A A	
gp190 ^s	AAGAACATCTCATAGTAAGATCGAAAAGCAGATCGAGACCGTTCTTGAGAAGACATTAAGAAGATGAAGAACAGCTGTGAGAAGAACAGATT	1800
AS	T K D E N K P D E K I L E V S D I V K V Q V Q R V U L L M N K	627
gp190 ⁿ	T A A A T T A A A A T C A A A T A T A T A T A T A	
gp190 ^s	ACAAAAAGACGAAAATAAACCAGATGAGAAGATECTGGAGGCTCTGGATATTCTTAAAGTCAGTCAGCAAGGTGCTCTCATGAACAACG	1890
AS	I D E L K K T Q L I L K N V E L K H N I H V P N S Y K Q E N	657
gp190 ⁿ	C T A A T G T A A T A A A T A A A T C T C T C C A A A A	
gp190 ^s	ATTGATGAAGTCAAGAAGACTCAACTCACTCTGAAAGAAGCTGGAGTTAAACATAATACATGTGCCAATAGTATAACCAGGAGAAAT	1980
AS	K Q E P Y Y L I V L K K E I D X L K V F M P K V E S L I N E	687
gp190 ⁿ	A A T T T T A T G T G A A A T T T A A T G A A T C A T A T	
gp190 ^s	AAGCAGGAACCATACTACCTCATCGTACTCAAGAAAGAGATAGACAAACTCAAAGTGTATGCCAAAGTCAGACGCCCTCATCAACGAA	2070
AS	E K K N I K T E G Q S D N S E P S T E G E I T G O A T T K P	717
gp190 ⁿ	A A A A A A T A G T G A A A C A A A A A A T A A T	
gp190 ^s	GAGAAGAACACATAAAACTGAAGGACACTCGAGATAACTCCGACCTTCACACAGAGAGAGATAACCGGACAGGCTACACCAAGCCC	2160
AS	G Q Q A G S A L E G D S V Q A Q A Q E Q K Q A Q P P V P V P	747
gp190 ⁿ	A A A T T A A T C A	
gp190 ^s	GGACAACAGGCCGGTTCAAGCTCTCGAAGGCCATAGCGTCAAGCTCAAGCAGACAGCAGGCCACAGCTCGACTGCCACTGCC	2250
AS	V P E A K A Q V P T P P A P V N N K T E N V S K L D Y L E K	777
gp190 ⁿ	A A A A A C A A A A T A T A T T C T A T T A A A A A A A A A A	
gp190 ^s	GTTCAGAGCTTAAGCTCAAGTGCCTACACCACCGCTCTGTGAATAACAGACCGAGAAATGTCAAGCAACTGGACTACTTGAGAAG	2340
AS	L Y E F L N T S Y I C H K Y I L V S E S T M N E R I L K Q Y	807
gp190 ⁿ	T A A T T A T A T A T T G T A T C A A A T A A T A A T	
gp190 ^s	CTCTATGAGTCTCTGAAATACATCTCATCTCCACAAAATATATCTCTCTCACAGCACTATGAACCGAGAGATTTAAACAGTAC	2430
AS	K I T K E E E S K L S S C D P L D L L F N I Q N N I P V H Y	837
gp190 ⁿ	A T A G A C T A A G T A T A T A T A A T A A T A A T A A T A	
gp190 ^s	AAGATAACCAAGGAAGAGGAGACTAACTCTCTCTCAACTCTCATGGAGATATGAGAAGGGAGATGGCTCGAACCTGTATAAACCTCAA	2520
AS	S M F D S L N N S L S Q L F M E I Y E K E M V C N L Y K L K	867
gp190 ⁿ	T T A A G T A A A T A T A A A A T T T T A T A T G	
gp190 ^s	TCTATGTTGAGCTCAACAAATTCTCTCTCAACTCTCATGGAGATATGAGAAGGGAGATGGCTCGAACCTGTATAAACCTCAA	2610
AS	D N D K I K N L L E E A K K V S T S V K T L S S S S M Q P L	897
gp190 ⁿ	T T A A T T A T A G A A A A A T A A G T C A A T A T A	
gp190 ^s	GACACCGACAAAGATTAAGAACCTCTGGAGGAACCTAAGAAGGTCTCACCTCTGTAAAACCTCTCTCTCCAGCTCCATGCAACCACTG	2700
AS	S L T P Q D K P E V S A N D D O T S H S T N L N N S L K L F E	927
gp190 ⁿ	A T A G T A A A T T T A A T T A T T G T A G T A T A A T A	
gp190 ^s	TCTCTCACACCTCAAGACAAGCCGAGTGGCCCTAACQACGACACCTCTCACTCGACCAACCTTAACACTCACTGAAACTGTTGAG	2790
AS	N I L S L G K N K N I Y Q E L I G Q K S S E N F Y E K I L K	957
gp190 ⁿ	A T A G T A A C A T A T A A T A A T A A G T A T A T A T A	
gp190 ^s	AACATCTCTCTCTGGCAAGAATAAGAACATCTACCAAGAACCTATTGGACAGAAATCTGCGAGAACCTCTACCGAGAACATGAAA	2880
AS	D S D T F Y N E S F T N F V K S K A D D I N S L N D E S K R	987
gp190 ⁿ	T T T T T A T C T T A T T A T A T T A T T T T A T G T A A G	
gp190 ^s	GACACCGACACATTCTATAACGAGACCTTCACTAACTCTGTAAAACGCCATGATATCACTCTCTAACGATGAACTCTAAACGTT	2970
AS	K K L E E D I N K L K K T L Q L S F D O L Y N K Y K L K L E R	1017
gp190 ⁿ	A T A A T T A T A A A A T T A T T A T T A T A T A T A T A T A	
gp190 ^s	AGAACGCTGGAGAGGACATCAATAACGCTGAAGAACAGACTCGAACACTGAGCTTCGACCTGTACACAAGTACACAAACTGAAACTGGAGAGA	3060
AS	L F D K K K T V G R Y K M Q I K R L T L L K E Q L E S K L N	1047
gp190 ⁿ	T A T T A A T T A A A T A A A C T T A T A A A A A T A T C A T G T	
gp190 ^s	CTCTTCGACAAAGAAGAACAGCTGGCAACTATAAGATGGCAGATCAAGAACCTGTGTTCTCACGGACGAGTTGAAAGCAAACCTCAAC	3150
AS	S L N N P K H V L Q N F S V F F N K K K E A E I A E T E N T	1077
gp190 ⁿ	T T C A G T T A A T T T T A A A A A T A A A A T A A	
gp190 ^s	TCACTGAAACAATCCGAAACACACTACTCCAGAACCTCTCACTGTTCAACAGAACAGGAAGGGAGATCCCGAGACAGAACACT	3240
AS	L E N T K I L L K E Y K G L V K Y Y N G E S S P L K T L S E	1107
gp190 ⁿ	T A A A A A T A T G T T A T A T A T A T A T A A T A A T A A T A	
gp190 ^s	CTGGAGAACACCAAGATCTCTCAACACTACAAGGCCGTCAGTATTATAATGGAGCTCTCTGAAAGACTCTCTCCGAG	3330
AS	E S I Q T E D N Y A S L E N F K V L S K L E G K L K D N L N	1137
gp190 ⁿ	A T C A T A A A T T T T A A T A A T A A T A A T A A T T A T	
gp190 ^s	GAGAGCATCCAGACCCAGGATAACTAGCCAGCCCTCGAGAACCTCAAGGTCTCTTAAGCTGAAAGCAAGCTGAAGGACACCTGAAC	3420

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AS	L E K K K L S Y L S S G L B H L I A E L K E V I K N K N Y T	1167
gp190 ⁿ	T A A A A T ATCA TA A T TA TT A T T ATA A A A A T A T T A	
gp190 ^s	CTGGAGAAGAAGAAGCTCAGCTACCTCTAGCGGACTGCATCACCTGATGCCGAGGTCAAGGAAGTCATTAAGAACAGAACTACACC	3510
AS	G N S P S E N N T D V N N A L E S Y K K F L P E G T D V A T	1197
gp190 ⁿ	T TCT T A G T T C T TA A A T C A A T A A	
gp190 ^s	GGCAATAGCCCAGCCAGAATAATACACGTGAATAACCCACTGGAACTTACAAGAAGTTCTGCCTGAAAGGAACAGATGTGCCCACT	3600
AS	V V S E S G S D T L E Q S O P K K P A S T H V G A E S N T I	1227
gp190 ⁿ	T AAG AG A T A A A A A A A A A A A A A A T C A	
gp190 ^s	GTGGTCTGAACTGGCTCCGACACATGGAGCAGTCACCTAAAGAGCCTGCATCTACTCATGGAGCCGACTTCACATTACATT	3690
AS	T T S Q N V D D E V D D V I X V P I F G E S E E D Y D D L G	1257
gp190 ⁿ	A A A T T A A A A A A A A A A A A T C A A T T T T A A	
gp190 ^s	ACCACATTCAGAACGTCGACGATGAGTCGATGACSTCATCTGCTCATCTGGCCGAGAGGAGGACTACCGATGACCTGGC	3780
AS	Q V V T G E A V T P S V I D N I L S K I E N E Y E V L Y L K	1287
gp190 ⁿ	A A A A A A A A A A A A A A A A T T T A T T T G T T A A	
gp190 ^s	CAGGTGGTCACCGGTGAGGCTGTCACTCTTCCGTGATGATAACATTCTGTCACAAAGAACGAACTGAGTCATCTGAA	3870
AS	P L A G V Y R S L K K Q L E N N N V M T F N V N V K D I L N S	1317
gp190 ⁿ	T A T T A A G T A A A T A A A T A T T T T T A T C A	
gp190 ^s	CCTCTGGCAGGGCTCTATAGCTCTCAAGAACAGCTGGAGAATAACGTGATGACCTTCATGTCACCTGAAGGACATTCTGAAACAGC	3960
AS	R F N K R E N F K N V L E S D L I P Y K D L E T S S N Y V V K	1347
gp190 ⁿ	A A C T A T T A ATCA T A A A T A A A A A G T T A	
gp190 ^s	CGCTTAATAAGAGAGAAAATTCAAGAACGTCCTGGAGAGGACTTGATCCCTATAAGACCTGACCTCTCTAACTACCTGTCAG	4050
AS	D P Y K F L N K E K R D K F L S S Y N Y I K D S I D T D I N	1377
gp190 ⁿ	T T A T T A A A A CT AAC C T T A T T A A T G A	
gp190 ^s	GACCCATACAAGTCCTCAATAAGAGAGAGGGATAAATTCTGTCAGTACAATATCAAGGACTCCATCGACACCGATATCAAT	4140
AS	F A N D V L G Y Y K I L S E K Y K S D L D S I K K Y I N D K	1407
gp190 ⁿ	T A T T A T A A T ATCA T A A A T A A A C A	
gp190 ^s	TTGGCTAATGATGTCCTGGGTATTACAAGATCTGAGCCAAAATACAAGTCTGACCTTGACTCTTAAAGATATCAACGATAAG	4230
AS	Q G E N E K Y L P F L N N I E T L Y K T V N D K I D L F V I	1437
gp190 ⁿ	T A G C T T A C T T G T A T A T T T T T T A T	
gp190 ^s	CAAGGGAGAACATGAAAATATCTGGCTCTGAAATACATGAAACCTGTACAGAACGTCAGGACAAAATCGACCTCTGTAATT	4320
AS	H L E A K V L N Y T Y E K S N V Z V K I K E L N Y L K T I Q	1467
gp190 ⁿ	TT A A A A T A T A T ATCA C A A A A T T T A T T	
gp190 ^s	CACCTGGAGGCCAACGTCCTCAACTATACTTACGAGAACGCAATGTGAAACTAAAATCAAGGAGCTGAACTACCTCAAACATCCAA	4410
AS	D K L A D F K K N N N F V G I A D L S T D Y N H N N L L T K	1497
gp190 ⁿ	AT T A T T T T T T A A A T T T C T A T A	
gp190 ^s	GACAAGCTGGCAGATTCAAGAAAAATAACAATTCTCGGAATTGCAACCTGTCTACCGATTATAACCCAACAATCTGTGACCAAG	4500
AS	F L S T G M V F E N L A K T V L S N L L D G N L Q G H L N I	1527
gp190 ⁿ	C T A G T A T T T T T T C T T A C T T A T T A T A T A T	
gp190 ^s	TTTCCTGTCACTGGCATGGTTGGAAAAACCTGCCAAAACAGTGTGCTGAGCAATCTGCTGAGGCCAACCTGCAAGGOCATGTCAGACATC	4590
AS	S Q H Q C V K K Q C P Q N S G C F R E L D E R E E C K C L L	1557
gp190 ⁿ	A A A A A T A A A T C T A A T A T A A A T A T A T A T A	
gp190 ^s	TCCCAGCACCAATCCGTGAAGAACAGTCCTCCAGAACAGCGCTGTTCAAGGACATGGAGCCGAAGAGTCAGTCCTCTG	4680
AS	N Y K Q E G D K C V E N P N P T C N E N N G C D A D A K C	1587
gp190 ⁿ	T T A T T A T T T T C T C T A T A C T	
gp190 ^s	AACTACAACAGAACGGAGATAAGTCGTGGAGAACCCAAACCTACCTGCAATGAAACATGGCGGTGTGACGCCGATGCCAAATGCC	4770
AS	T E E D S G S N G K K I T C E C T K P D S Y P L F D G I F C	1617
gp190 ⁿ	A T T C A T A C C T A A T T T T T T T C	
gp190 ^s	ACCGAGGAAGACACGGCTCTAACGAAAGAAAATCACATGGAGTCATAAGCCGACTCTATCCACTCTTCGACGCCGATTTTGC	4860
AS	S S S N F L G I F F L L I L M L I L Y S F I * * * * * 1639	
gp190 ⁿ	AGTTTC T A A A C A T A T A A T A A T A T A T T T	
gp190 ^s	TCCAGCTATAATTCTGGCACTCTCTCTGATCTCATGCTGATCTGTACAGCTCATCTAAAGATGATGCG	4940
	stop codon Clal	

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Fig. 3D

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N'-terminus

N'-terminus

gp190s1 Sequence

DNA Sequence	AA Sequence	AA Position	
GC <u>ACGCG</u> GATGAAAATC			AGCTCTAATTAAATA <u>AGCGGGCC</u> CATCGATGGC
Mlu I	Met Lys Ile	1 2 3	Ser Ser Asn stop codon Not I
			Cla I 1619 1620 1621

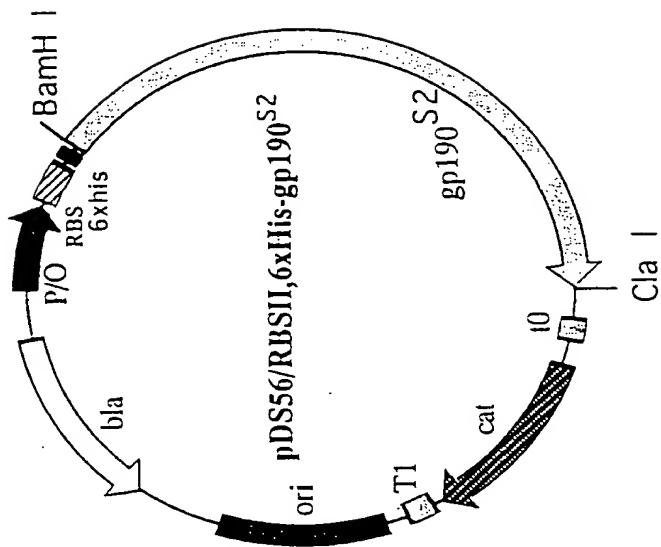
gp190s2 Sequence

DNA Sequence	AA Sequence	AA Position	
GC <u>GGATCC</u> GTGACCCAC			AGCTCTAATTAAATA <u>AGCGGGCC</u> CATCGATGGC
BamH I	Val Thr His	20 21 22	Ser Ser Asn stop codon Not I
			Cla I 1619 1620 1621

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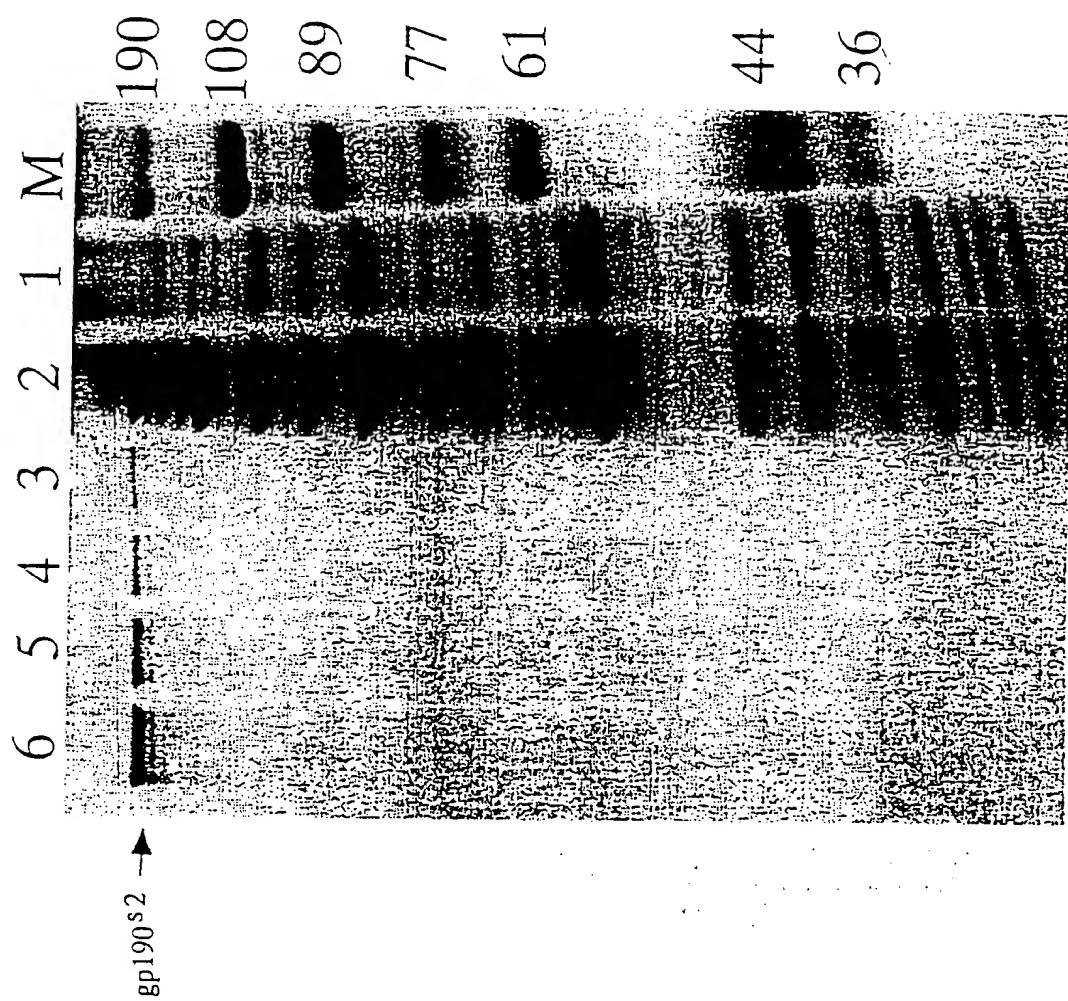
Fig. 4A



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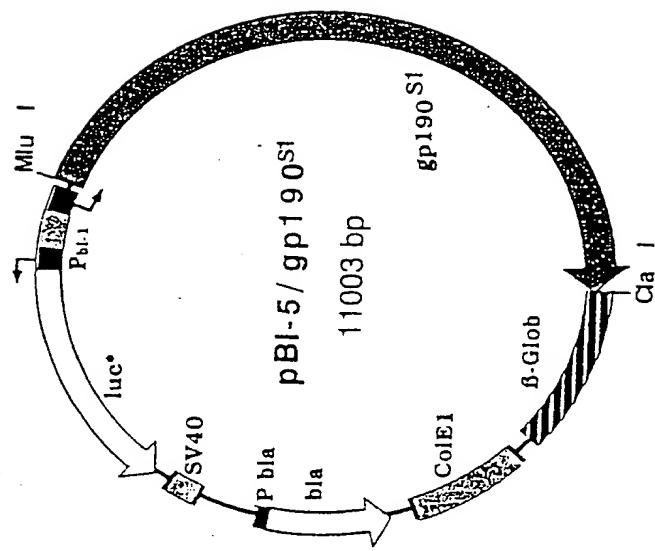
Fig. 4B



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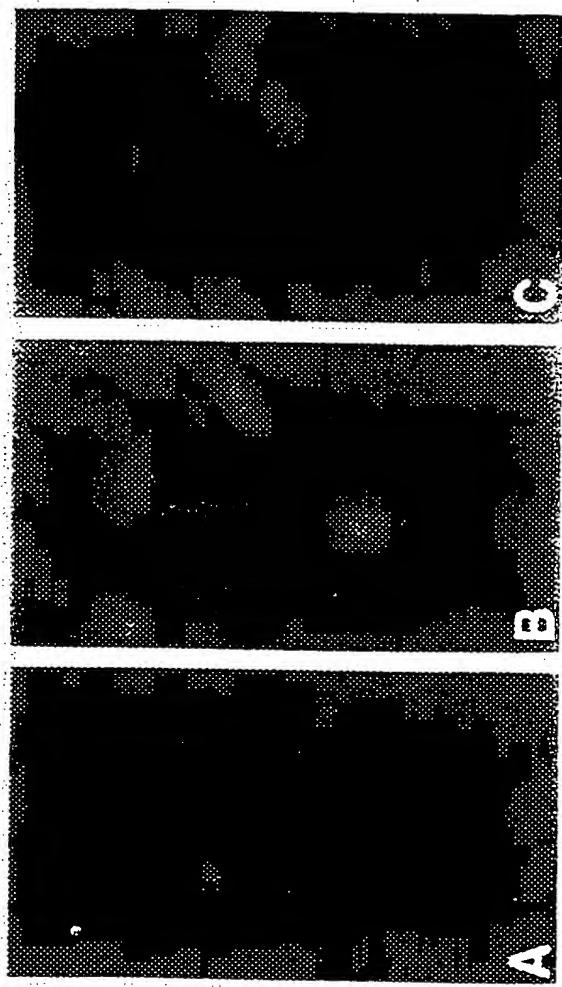
Fig. 5A



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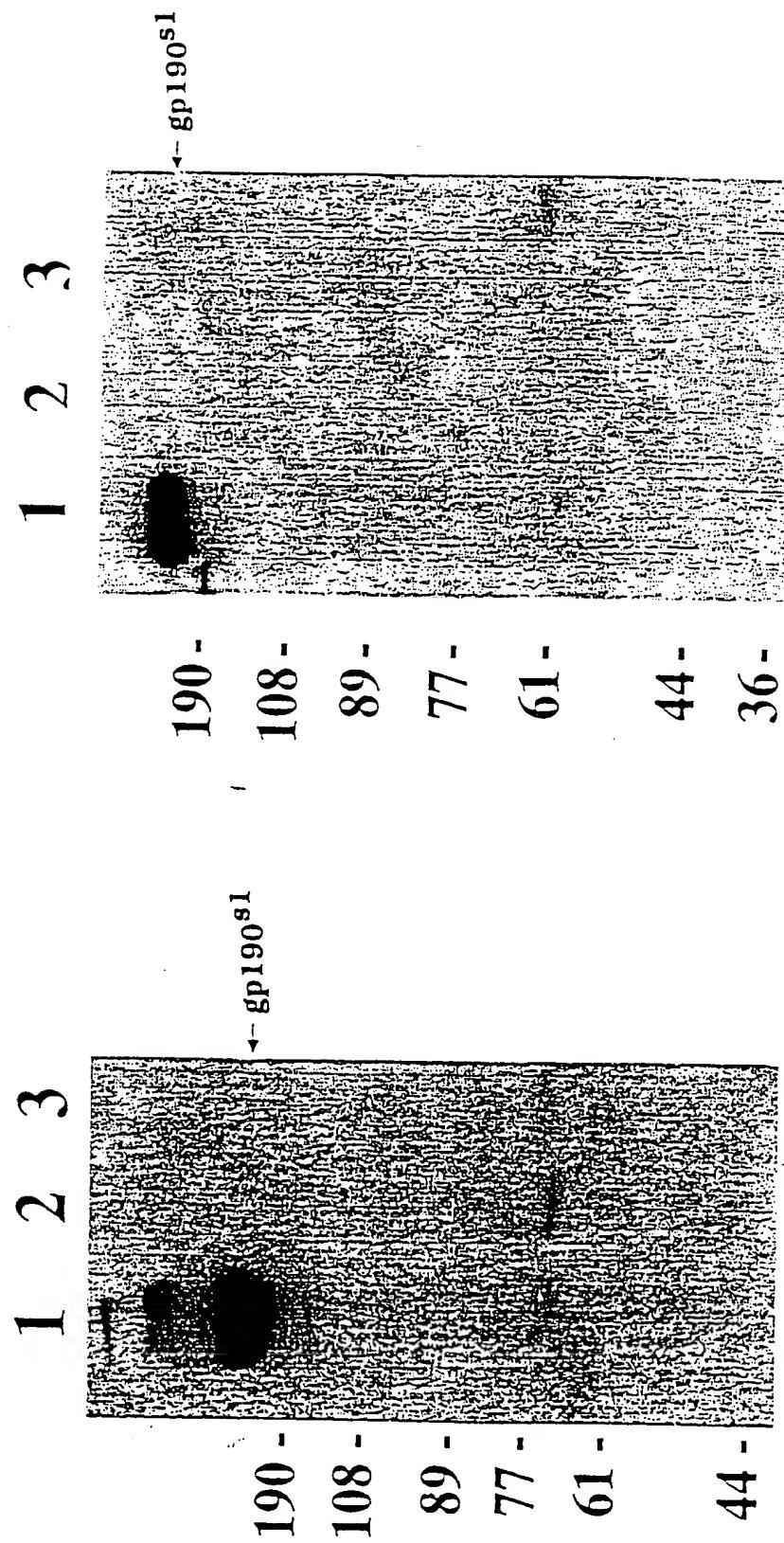
Fig. 5B



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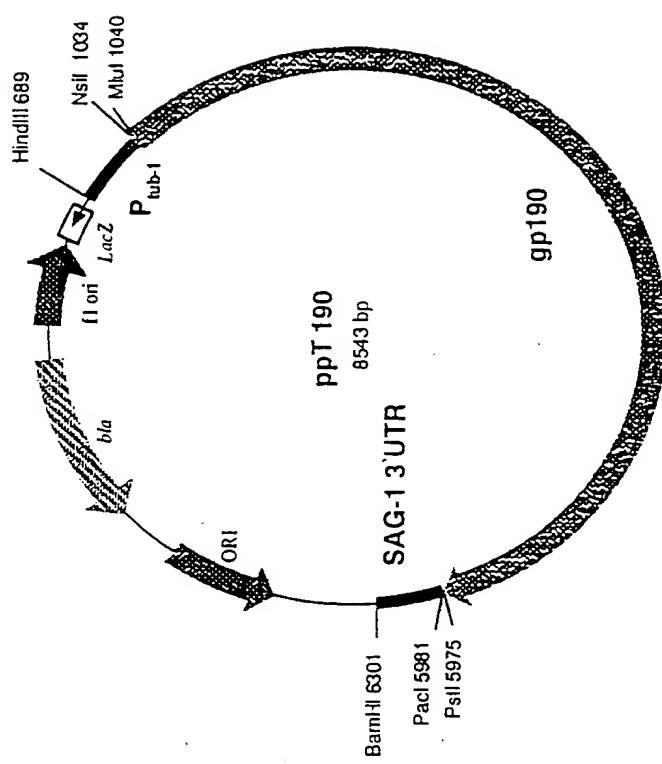
Fig. 5C



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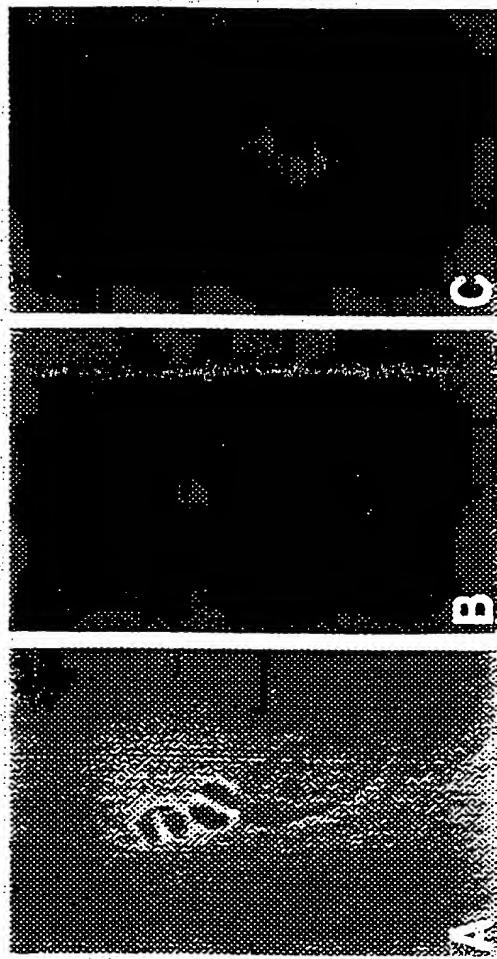
Fig. 6A



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Fig. 6B



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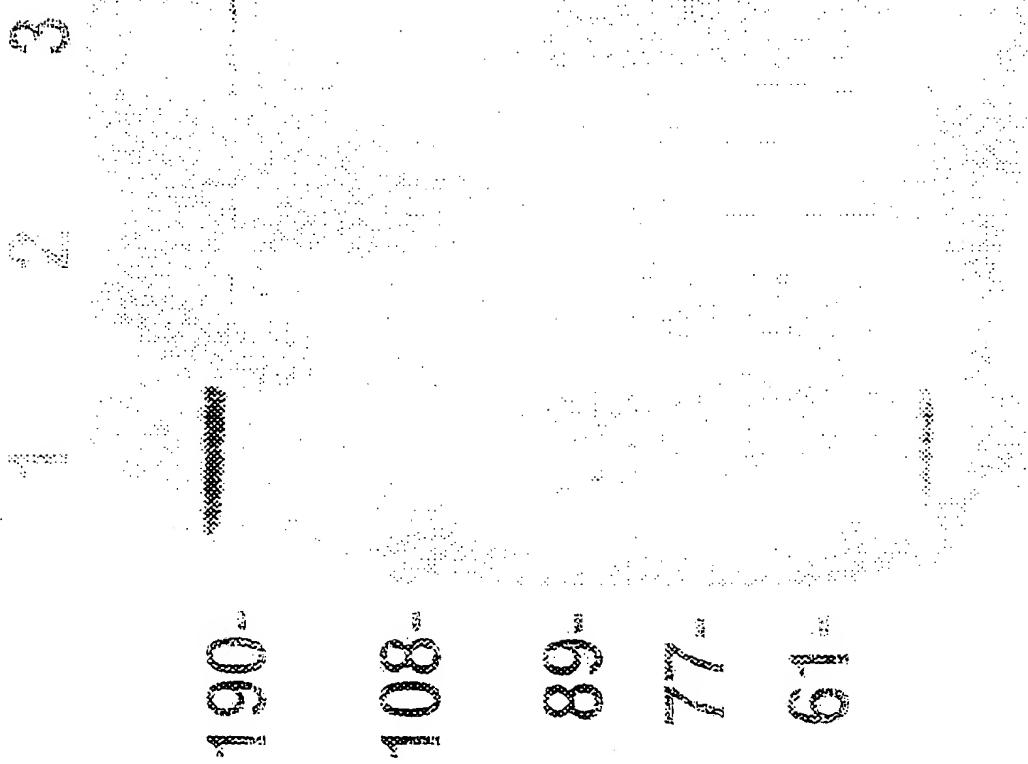


Fig. 6c